



NCBI

Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

EXHIBIT

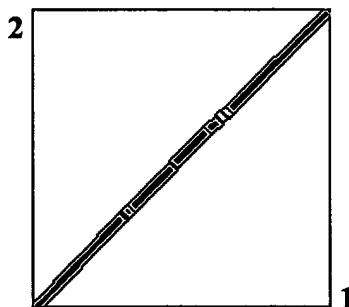
B

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix **BLOSUM62** gap open:**11** gap extension:**1**x_dropoff: **50** expect: **10.000** wordsize: **3** Filter Align

Sequence 1 lcl|seq_1 Length 862 (1 .. 862)

Sequence 2 lcl|seq_2 Length 859 (1 .. 859)



BEST AVAILABLE COPY

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 1202 bits (3110), Expect = 0.0

Identities = 637/869 (73%), Positives = 704/869 (80%), Gaps = 17/869 (1%)

Query: 1 MERAESSSTEPAKAIPIDRKSVHQICSGQVVLSSLSTAVKELVENSLDAGATNIDLKLKD 60
ME+ E STE AKAIPID KSVHQICSGQV+LSLSTAVKEL+ENS+DAGAT IDL+LKD

Sbjct: 1 MEQTEGVSTECAKAIPIDGKSVHQICSGQVILSLSTAVKELIENSVDAGATTIDLRLKD 60

Query: 61 YGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADELTQVETFGFRGEALSSLCALSDV 120
YGVDLIEVSDNGCGVEEENFEGL LKHHTSKIQEFADELTQVETFGFRGEALSSLCALSDV

Sbjct: 61 YGVDLIEVSDNGCGVEEENFEGLALKHHTSKIQEFADELTQVETFGFRGEALSSLCALSDV 120

Query: 121 TISTCHASAKVGTRLFDHNGKIIQKTPYPRPRGTTVSVQQLFSTLPVRHKEFQRNIKKE 180
TISTCH SA VGTRL+FDHNGKII QKTPYPRP+GTTVSVQ LF TLPVR+KEFQRNIKKE

Sbjct: 121 TISTCHGSASVGTRLVDHNGKITQKTPYPRPKGTTVSVQHLFYTLPVRYKEFQRNIKKE 180

Query: 181 YAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCTGGSPSIKENIGSVFGQKQLQSLI 240
Y+KMVQVL AYCIIISAG+RVSCTNQLGQGKR VVCT G+ +KENIGSVFGQKQLQSLI

Sbjct: 181 YSKMVQVLQAYCIISAGRVRSCTNQLGQGKRHAVVCTS GTSGMKENIGSVFGQKQLQSLI 240

Query: 241 PFVQLPPSDSVCEEYGLSCDALHNLF--YISGFISQCTHGVGRSSTDQFFFINRRPCD 298
PFVQLPPSD+VCEEYGLS S H F + + F S T G T F R P

Sbjct: 241 PFVQLPPSDAVCEEYGLSTSGR-HKTFSTFRASFHSARTAPGGVQQTG-SFSSSIRGPVT 298

Query: 299 PAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLLAVLKTS 358
+ L YHMYNRHQYPFVVLN+SVDSECVDINVTPDKRQILLQEEKLLLAVLKTS

Sbjct: 299 QRSLSLSMRFYHMYNRHQYPFVVLNVSDSECVDINVTPDKRQILLQEEKLLLAVLKTS 358

Query: 359 LIGMFDSDVNLNVQQPLLDVEGNLIKMAADLEKPMVEKQDQSPSLR-TGEEKKDVI 417
LIGMFDS D NKLNV+QQPLLDVEGNL+K+H A+LEKP+ KQD SPSL+ T +EK+ SI

Sbjct: 359 LIGMFDSANKLNVNQQPLLDVEGNLVKLHTAELEKPVPGKQDNSPSLKSTADEKRVASI 418

Query: 418 SRLREAFSLRHTTENKPHSPKTPEPRRSPLGQKRGMLSSSTSGAISDKGVLRPQKEAVSS 477
SRLREAFSL T E K P+T E RS +KRG+LSS S IS +G+ Q + VS

Sbjct: 419 SRLREAFSLHPTKEIKSRGPETAEALTRSFPEKRGVLSSYPSDVISYRGLRGSQDKLVSP 478

Query: 478 SHGPSDPTDRAEVEKDGHGSTVDSEG-FSIPDTGSHCSSEYAASSPGDRGSQEHVDSQ 536
+ P D DR ++EKDSG STS SE FS P+ S SS+Y SS DR SQE ++

Sbjct: 479 TDSPGDCMDREKIEKDGLSSTSAGSEEEFSTPEVASSFSSDYNVSSLEDRPSQETINCG 538

Query: 537 E---KAPETDDSFSDVDCHSNQEDTGCKFRVLQPPTNLATPNTKRFKKEEILSSSDICQK 593
+ + P T S ED G + + LP L+ N KRFK EE S+ +I Q+

Sbjct: 539 DLDCRPPGTGQLKP-----EDHGYQCKALPL-ARLSPTNAKRFKTEERPSNVNISQR 590

Query: 594 LVNTQDMASASQVDVAVKINKKVPLDFSMSSLAKRIKQLHHEAQSEQGEQNYRKFRASIC 653
L Q SA++VDVA+K+NK++V L+FS+SSLAKR+KQL H Q++ E +YRKFRASIC

Sbjct: 591 LPGPQSTSAAEVDAIKMNRIVLLEFSLSSLAKRMQLQHLKAQNKHESYRKFRASIC 650

Query: 654 PGENQAAEDELRKEISKTMFAEMEIIGQFNLFIIITKLNEIFVTDQHATDEKYNFEMLQ 713
PGENQAAEDELRKEISK+MFAEMEI+GQFNLFII+TKL ED+F+VDQHA DEKYNFEMLQ

Sbjct: 651 PGENQAAEDELRKEISKSMFAEMEIILGQFNLFIVTKLKEDLFLVDQHAADEKYNFEMLQ 710

Query: 714 QHTVLQGQRLIAPQTNLNTAVNEAVLIENLEIFRKNGFDFVIDENAPVTERAKLISLPTS 773
QHTVLQ QRLI QTNLNTAVNEAVLIENLEIFRKNGFDFVIDE+APVTERAKLISLPTS

Sbjct: 711 QHTVLQAQRLITPQTNLNTAVNEAVLIENLEIFRKNGFDFVIDEADAPVTERAKLISLPTS 770

Query: 774 KNWTFGPQDVDELIFMLSDSPGVMCRPSRVKQMFASRACRKSVMITGALTSEMKKLITH 833
KNWTFGPQD+DELIFMLSDSPGVMCRPSRV+QMFASRACRKSVMITGALT SEMKKLITH

Sbjct: 771 KNWTFGPQDDIDEELIFMLSDSPGVMCRPSVRQMFASRACRKSVMITGALTNASEMKKLITH 830

Query: 834 MGEMDHPWNCPHGRPTMRHIANLGVISQN 862

MGEMDHPWNCPHGRPTMRH+ANL VISQN

Sbjct: 831 MGEMDHPWNCPHGRPTMRHVANLDVISQN 859

CPU time: 0.17 user secs. 0.04 sys. secs 0.21 total secs.

Lambda	K	H
0.315	0.131	0.371

Gapped

Lambda	K	H
0.267	0.0410	0.140

BEST AVAILABLE COPY

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 6158

Number of Sequences: 0

Number of extensions: 502

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 859

length of database: 461,760,005

effective HSP length: 136

effective length of query: 723

effective length of database: 461,759,869

effective search space: 333852385287
effective search space used: 333852385287
T: 9
A: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.6 bits)
S2: 79 (35.0 bits)

BEST AVAILABLE COPY